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RAW SEQUENCE LISTING

DATE: 01/19/2002

PATENT APPLICATION: US/09/822,682

TIME: 11:17:21

Input Set : A:\10448-051002.txt

Output Set: N:\CRF3\01192002\I822682.raw

ENTERED

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4 <110> APPLICANT: Detmar, Michael J.
5      Streit, Michael
7 <120> TITLE OF INVENTION: THROMBOSPONDIN-2 AND USES THEREOF
9 <130> FILE REFERENCE: 10287-051002
11 <140> CURRENT APPLICATION NUMBER: 09/822,682
12 <141> CURRENT FILING DATE: 2001-03-30
14 <150> PRIOR APPLICATION NUMBER: 09/536,087
15 <151> PRIOR FILING DATE: 2000-03-24
17 <150> PRIOR APPLICATION NUMBER: 60/127,221
18 <151> PRIOR FILING DATE: 1999-03-31
20 <160> NUMBER OF SEQ ID NOS: 11
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3596
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (26)...(3541)
33 <400> SEQUENCE: 1
34 caggagctca gctgcaggag gcagg atg gtc tgg agg ctg gtc ctg ctg gct      52
35                               Met Val Trp Arg Leu Val Leu Leu Ala
36                               1               5
38 ctg tgg gtg tgg ccc agc acg caa gct ggt cac cag gac aaa gac acg      100
39 Leu Trp Val Trp Pro Ser Thr Gln Ala Gly His Gln Asp Lys Asp Thr
40 10                15                20                25
42 acc ttc gac ctt ttc agt atc agc aac atc aac cgc aag acc att ggc      148
43 Thr Phe Asp Leu Phe Ser Ile Ser Asn Ile Asn Arg Lys Thr Ile Gly
44                30                35                40
46 gcc aag cag ttc cgc ggg ccc gac ccc ggc gtg ccg gct tac cgc ttc      196
47 Ala Lys Gln Phe Arg Gly Pro Asp Pro Gly Val Pro Ala Tyr Arg Phe
48                45                50                55
50 gtg cgc ttt gac tac atc cca ccg gtg aac gca gat gac ctc agc aag      244
51 Val Arg Phe Asp Tyr Ile Pro Pro Val Asn Ala Asp Asp Leu Ser Lys
52 60                65                70
54 atc acc aag atc atg cgg cag aag gag ggc ttc ttc ctc acg gcc cag      292
55 Ile Thr Lys Ile Met Arg Gln Lys Glu Gly Phe Phe Leu Thr Ala Gln
56 75                80                85
58 ctc aag cag gac ggc aag tcc agg ggc acg ctg ttg gct ctg gag ggc      340
59 Leu Lys Gln Asp Gly Lys Ser Arg Gly Thr Leu Leu Ala Leu Glu Gly
60 90                95                100                105
62 ccc ggt ctc tcc cag agg cag ttc gag atc gtc tcc aat ggc ccc gcg      388
63 Pro Gly Leu Ser Gln Arg Gln Phe Glu Ile Val Ser Asn Gly Pro Ala

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64	110	115	120	
66	gac acg ctg gat ctc acc tac tgg att gac ggc acc cgg cat gtg gtc	436		
67	Asp Thr Leu Asp Leu Thr Tyr Trp Ile Asp Gly Thr Arg His Val Val			
68	125 130 135			
70	tcc ctg gag gac gtc ggc ctg gct gac tcg cag tgg aag aac gtc acc	484		
71	Ser Leu Glu Asp Val Gly Leu Ala Asp Ser Gln Trp Lys Asn Val Thr			
72	140 145 150			
74	gtg cag gtg gct ggc gag acc tac agc ttg cac gtg ggc tgc gac ctc	532		
75	Val Gln Val Ala Gly Glu Thr Tyr Ser Leu His Val Gly Cys Asp Leu			
76	155 160 165			
78	ata gac agc ttc gct ctg gac gag ccc ttc tac gag cac ctg cag gcg	580		
79	Ile Asp Ser Phe Ala Leu Asp Glu Pro Phe Tyr Glu His Leu Gln Ala			
80	170 175 180 185			
82	gaa aag agc cgg atg tac gtg gcc aaa ggc tct gcc aga gag agt cac	628		
83	Glu Lys Ser Arg Met Tyr Val Ala Lys Gly Ser Ala Arg Glu Ser His			
84	190 195 200			
86	ttc agg ggt ttg ctt cag aac gtc cac cta gtg ttt gaa aac tct gtg	676		
87	Phe Arg Gly Leu Leu Gln Asn Val His Leu Val Phe Glu Asn Ser Val			
88	205 210 215			
90	gaa gat att cta agc aag aag ggt tgc cag caa ggc cag gga gct gag	724		
91	Glu Asp Ile Leu Ser Lys Lys Gly Cys Gln Gln Gly Gln Gly Ala Glu			
92	220 225 230			
94	atc aac gcc atc agt gag aac aca gag acg ctg cgc ctg ggt ccg cat	772		
95	Ile Asn Ala Ile Ser Glu Asn Thr Glu Thr Leu Arg Leu Gly Pro His			
96	235 240 245			
98	gtc acc acc gag tac gtg ggc ccc agc tca gag agg agg ccc gag gtg	820		
99	Val Thr Thr Glu Tyr Val Gly Pro Ser Ser Glu Arg Arg Pro Glu Val			
100	250 255 260 265			
102	tgc gaa cgc tcg tgc gag gag ctg gga aac atg gtc cag gag ctc tcg	868		
103	Cys Glu Arg Ser Cys Glu Glu Leu Gly Asn Met Val Gln Glu Leu Ser			
104	270 275 280			
106	ggg ctc cac gtc ctc gtg aac cag ccc agc gag aac ctc aag aga gtg	916		
107	Gly Leu His Val Leu Val Asn Gln Pro Ser Glu Asn Leu Lys Arg Val			
108	285 290 295			
110	tcg aat gat aac cag ttt ctc tgg gag ctc att ggt ggc cct cct aag	964		
111	Ser Asn Asp Asn Gln Phe Leu Trp Glu Leu Ile Gly Gly Pro Pro Lys			
112	300 305 310			
114	aca agg aac atg tca gct tgc tgg cag gat ggc cgg ttc ttt gcg gaa	1012		
115	Thr Arg Asn Met Ser Ala Cys Trp Gln Asp Gly Arg Phe Phe Ala Glu			
116	315 320 325			
118	aat gaa acg tgg gtg gtg gac agc tgc acc acg tgt acc tgc aag aaa	1060		
119	Asn Glu Thr Trp Val Val Asp Ser Cys Thr Thr Cys Thr Cys Lys Lys			
120	330 335 340 345			
122	ttt aaa acc att tgc cac caa atc acc tgc ccg cct gca acc tgc gcc	1108		
123	Phe Lys Thr Ile Cys His Gln Ile Thr Cys Pro Pro Ala Thr Cys Ala			
124	350 355 360			
126	agt cca tcc ttt gtg gaa ggc gaa tgc tgc cct tcc tgc ctc cac tcg	1156		
127	Ser Pro Ser Phe Val Glu Gly Glu Cys Cys Pro Ser Cys Leu His Ser			
128	365 370 375			

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130	gtg	gac	ggt	gag	gag	ggc	tgg	tct	ccg	tgg	gca	gag	tgg	acc	cag	tgc	1204
131	Val	Asp	Gly	Glu	Glu	Gly	Trp	Ser	Pro	Trp	Ala	Glu	Trp	Thr	Gln	Cys	
132			380					385					390				
134	tcc	gtg	acg	tgt	ggc	tct	ggg	acc	cag	cag	aga	ggc	cgg	tcc	tgt	gac	1252
135	Ser	Val	Thr	Cys	Gly	Ser	Gly	Thr	Gln	Gln	Arg	Gly	Arg	Ser	Cys	Asp	
136			395				400					405					
138	gtc	acc	agc	aac	acc	tgc	ttg	ggg	ccc	tcc	atc	cag	aca	cgg	gct	tgc	1300
139	Val	Thr	Ser	Asn	Thr	Cys	Leu	Gly	Pro	Ser	Ile	Gln	Thr	Arg	Ala	Cys	
140	410					415					420					425	
142	agt	ctg	agc	aag	tgt	gac	acc	cgc	atc	cgg	cag	gac	ggc	ggc	tgg	agc	1348
143	Ser	Leu	Ser	Lys	Cys	Asp	Thr	Arg	Ile	Arg	Gln	Asp	Gly	Gly	Trp	Ser	
144					430					435					440		
146	cac	tgg	tca	cct	tgg	tct	tca	tgc	tct	gtg	acc	tgt	gga	gtt	ggc	aat	1396
147	His	Trp	Ser	Pro	Trp	Ser	Ser	Cys	Ser	Val	Thr	Cys	Gly	Val	Gly	Asn	
148					445				450					455			
150	atc	aca	cgc	atc	cgt	ctc	tgc	aac	tcc	cca	gtg	ccc	cag	atg	ggg	ggc	1444
151	Ile	Thr	Arg	Ile	Arg	Leu	Cys	Asn	Ser	Pro	Val	Pro	Gln	Met	Gly	Gly	
152			460					465					470				
154	aag	aat	tgc	aaa	ggg	agt	ggc	cgg	gag	acc	aaa	gcc	tgc	cag	ggc	gcc	1492
155	Lys	Asn	Cys	Lys	Gly	Ser	Gly	Arg	Glu	Thr	Lys	Ala	Cys	Gln	Gly	Ala	
156			475				480					485					
158	cca	tgc	cca	atc	gat	ggc	cgc	tgg	agc	ccc	tgg	tcc	ccg	tgg	tcg	gcc	1540
159	Pro	Cys	Pro	Ile	Asp	Gly	Arg	Trp	Ser	Pro	Trp	Ser	Pro	Trp	Ser	Ala	
160	490					495					500					505	
162	tgc	act	gtc	acc	tgt	gcc	ggg	atc	cgg	gag	cgc	acc	cgg	gtc	tgc		1588
163	Cys	Thr	Val	Thr	Cys	Ala	Gly	Gly	Ile	Arg	Glu	Arg	Thr	Arg	Val	Cys	
164					510					515					520		
166	aac	agc	cct	gag	cct	cag	tac	gga	ggg	aag	gcc	tgc	gtg	ggg	gat	gtg	1636
167	Asn	Ser	Pro	Glu	Pro	Gln	Tyr	Gly	Gly	Lys	Ala	Cys	Val	Gly	Asp	Val	
168					525					530					535		
170	cag	gag	cgt	cag	atg	tgc	aac	aag	agg	agc	tgc	ccc	gtg	gat	ggc	tgt	1684
171	Gln	Glu	Arg	Gln	Met	Cys	Asn	Lys	Arg	Ser	Cys	Pro	Val	Asp	Gly	Cys	
172					540					545					550		
174	tta	tcc	aac	ccc	tgc	ttc	ccg	gga	gcc	cag	tgc	agc	agc	ttc	ccc	gat	1732
175	Leu	Ser	Asn	Pro	Cys	Phe	Pro	Gly	Ala	Gln	Cys	Ser	Ser	Phe	Pro	Asp	
176					555					560					565		
178	ggg	tcc	tgg	tca	tgc	ggc	tcc	tgc	cct	gtg	ggc	ttc	ttg	ggc	aat	ggc	1780
179	Gly	Ser	Trp	Ser	Cys	Gly	Ser	Cys	Pro	Val	Gly	Phe	Leu	Gly	Asn	Gly	
180	570					575					580					585	
182	acc	cac	tgt	gag	gac	ctg	gac	gag	tgt	gcc	ctg	gtc	ccc	gac	atc	tgc	1828
183	Thr	His	Cys	Glu	Asp	Leu	Asp	Glu	Cys	Ala	Leu	Val	Pro	Asp	Ile	Cys	
184					590					595					600		
186	ttc	tcc	acc	agc	aag	gtg	cct	cgc	tgt	gtc	aac	act	cag	cct	ggc	ttc	1876
187	Phe	Ser	Thr	Ser	Lys	Val	Pro	Arg	Cys	Val	Asn	Thr	Gln	Pro	Gly	Phe	
188					605					610					615		
190	cac	tgc	ctg	ccc	tgc	ccg	ccc	cga	tac	aga	ggg	aac	cag	ccc	gtc	ggg	1924
191	His	Cys	Leu	Pro	Cys	Pro	Pro	Arg	Tyr	Arg	Gly	Asn	Gln	Pro	Val	Gly	
192					620					625					630		
194	gtc	ggc	ctg	gaa	gca	gcc	aag	acg	gaa	aag	caa	gtg	tgt	gag	ccc	gaa	1972

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195	Val	Gly	Leu	Glu	Ala	Ala	Lys	Thr	Glu	Lys	Gln	Val	Cys	Glu	Pro	Glu	
196		635					640					645					
198	aac	cca	tgc	aag	gac	aag	aca	cac	aac	tgc	cac	aag	cac	gcg	gag	tgc	2020
199	Asn	Pro	Cys	Lys	Asp	Lys	Thr	His	Asn	Cys	His	Lys	His	Ala	Glu	Cys	
200	650					655					660					665	
202	atc	tac	ctg	ggc	cac	ttc	agc	gac	ccc	atg	tac	aag	tgc	gag	tgc	cag	2068
203	Ile	Tyr	Leu	Gly	His	Phe	Ser	Asp	Pro	Met	Tyr	Lys	Cys	Glu	Cys	Gln	
204					670					675						680	
206	aca	ggc	tac	gcg	ggc	gac	ggg	ctc	atc	tgc	ggg	gag	gac	tcg	gac	ctg	2116
207	Thr	Gly	Tyr	Ala	Gly	Asp	Gly	Leu	Ile	Cys	Gly	Glu	Asp	Ser	Asp	Leu	
208				685					690					695			
210	gac	ggc	tgg	ccc	aac	ctc	aat	ctg	gtc	tgc	gcc	acc	aac	gcc	acc	tac	2164
211	Asp	Gly	Trp	Pro	Asn	Leu	Asn	Leu	Val	Cys	Ala	Thr	Asn	Ala	Thr	Tyr	
212			700					705					710				
214	cac	tgc	atc	aag	gat	aac	tgc	ccc	cat	ctg	cca	aat	tct	ggg	cag	gaa	2212
215	His	Cys	Ile	Lys	Asp	Asn	Cys	Pro	His	Leu	Pro	Asn	Ser	Gly	Gln	Glu	
216		715				720					725						
218	gac	ttt	gac	aag	gac	ggg	att	ggc	gat	gcc	tgt	gat	gat	gac	gat	gac	2260
219	Asp	Phe	Asp	Lys	Asp	Gly	Ile	Gly	Asp	Ala	Cys	Asp	Asp	Asp	Asp	Asp	
220	730				735					740						745	
222	aat	gac	ggt	gtg	acc	gat	gag	aag	gac	aac	tgc	cag	ctc	ctc	ttc	aat	2308
223	Asn	Asp	Gly	Val	Thr	Asp	Glu	Lys	Asp	Asn	Cys	Gln	Leu	Leu	Phe	Asn	
224				750					755						760		
226	ccc	cgc	cag	gct	gac	tat	gac	aag	gat	gag	gtt	ggg	gac	cgc	tgt	gac	2356
227	Pro	Arg	Gln	Ala	Asp	Tyr	Asp	Lys	Asp	Glu	Val	Gly	Asp	Arg	Cys	Asp	
228			765					770					775				
230	aac	tgc	cct	tac	gtg	cac	aac	cct	gcc	cag	atc	gac	aca	gac	aac	aat	2404
231	Asn	Cys	Pro	Tyr	Val	His	Asn	Pro	Ala	Gln	Ile	Asp	Thr	Asp	Asn	Asn	
232			780					785					790				
234	gga	gag	ggt	gac	gcc	tgc	tcc	gtg	gac	att	gat	ggg	gac	gat	gtc	ttc	2452
235	Gly	Glu	Gly	Asp	Ala	Cys	Ser	Val	Asp	Ile	Asp	Gly	Asp	Asp	Val	Phe	
236		795				800					805						
238	aat	gaa	cga	gac	aat	tgt	ccc	tac	gtc	tac	aac	act	gac	cag	agg	gac	2500
239	Asn	Glu	Arg	Asp	Asn	Cys	Pro	Tyr	Val	Tyr	Asn	Thr	Asp	Gln	Arg	Asp	
240	810				815					820						825	
242	acg	gat	ggt	gac	ggt	gtg	ggg	gat	cac	tgt	gac	aac	tgc	ccc	ctg	gtg	2548
243	Thr	Asp	Gly	Asp	Gly	Val	Gly	Asp	His	Cys	Asp	Asn	Cys	Pro	Leu	Val	
244				830					835						840		
246	cac	aac	cct	gac	cag	acc	gac	gtg	gac	aat	gac	ctt	gtt	ggg	gac	cag	2596
247	His	Asn	Pro	Asp	Gln	Thr	Asp	Val	Asp	Asn	Asp	Leu	Val	Gly	Asp	Gln	
248			845					850					855				
250	tgt	gac	aac	aac	gag	gac	ata	gat	gac	gac	ggc	cac	cag	aac	aac	cag	2644
251	Cys	Asp	Asn	Asn	Glu	Asp	Ile	Asp	Asp	Asp	Gly	His	Gln	Asn	Asn	Gln	
252			860					865					870				
254	gac	aac	tgc	ccc	tac	atc	tcc	aac	gcc	aac	cag	gct	gac	cat	gac	aga	2692
255	Asp	Asn	Cys	Pro	Tyr	Ile	Ser	Asn	Ala	Asn	Gln	Ala	Asp	His	Asp	Arg	
256		875				880					885						
258	gac	ggc	cag	ggc	gac	gcc	tgt	gac	cct	gat	gat	gac	aac	gat	ggc	gtc	2740
259	Asp	Gly	Gln	Gly	Asp	Ala	Cys	Asp	Pro	Asp	Asp	Asp	Asn	Asp	Gly	Val	

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260	890		895		900		905		
262	ccc	gat	gac	agg	gac	aac	tgc	cgg	ctt
263	Pro	Asp	Asp	Arg	Asp	Asn	Cys	Arg	Leu
264				910				915	
266	gac	ttg	gac	ggt	gat	gga	cgg	ggt	gat
267	Asp	Leu	Asp	Gly	Asp	Gly	Arg	Gly	Asp
268				925				930	
270	aac	gac	aac	atc	cca	gat	att	gat	gtg
271	Asn	Asp	Asn	Ile	Pro	Asp	Ile	Asp	Asp
272				940				945	
274	atc	agt	gag	aca	gac	ttc	agg	aac	ttc
275	Ile	Ser	Glu	Thr	Asp	Phe	Arg	Asn	Phe
276				955				960	
278	aaa	ggg	acc	acc	caa	att	gat	ccc	aac
279	Lys	Gly	Thr	Thr	Gln	Ile	Asp	Pro	Asn
280	970							975	
282	aag	gag	ctg	gtt	cag	aca	gcc	aac	tcg
283	Lys	Glu	Leu	Val	Gln	Thr	Ala	Asn	Ser
284								990	
286	ttt	gac	gag	ttt	ggg	tct	gtg	gac	ttc
287	Phe	Asp	Glu	Phe	Gly	Ser	Val	Asp	Phe
288				1005				1010	
290	act	gac	cgg	gac	gac	gac	tat	gcc	ggc
291	Thr	Asp	Arg	Asp	Asp	Tyr	Ala	Gly	Phe
292				1020				1025	
294	agc	agc	cgc	ttc	tat	gtg	gtg	atg	tgg
295	Ser	Ser	Arg	Phe	Tyr	Val	Val	Met	Trp
296				1035				1040	
298	tgg	gag	gac	cag	ccc	acg	cgg	gcc	tat
299	Trp	Glu	Asp	Gln	Pro	Thr	Arg	Ala	Tyr
300	1050							1055	
302	aag	gtg	gtg	aac	tcc	acc	acg	ggg	acg
303	Lys	Val	Val	Asn	Ser	Thr	Thr	Gly	Thr
304				1070				1075	
306	ctg	tgg	cac	acg	ggg	aac	acg	ccg	ggg
307	Leu	Trp	His	Thr	Gly	Asn	Thr	Pro	Gly
308				1085				1090	
310	gac	ccc	agg	aac	att	ggc	tgg	aag	gac
311	Asp	Pro	Arg	Asn	Ile	Gly	Trp	Lys	Asp
312				1100				1105	
314	ctg	act	cac	agg	ccc	aag	acc	ggc	tac
315	Leu	Thr	His	Arg	Pro	Lys	Thr	Gly	Tyr
316				1115				1120	
318	gga	aaa	cag	gtc	atg	gca	gac	tca	gga
319	Gly	Lys	Gln	Val	Met	Ala	Asp	Ser	Gly
320	1130							1135	
322	gct	ggc	ggg	cgg	ctg	ggt	cta	ttt	gtc
323	Ala	Gly	Gly	Arg	Leu	Gly	Leu	Phe	Val
324				1150				1155	

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